

OIKE

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/804,474A

TIME: 12:33:31

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\08162001\I804474A.raw

4 <110> APPLICANT: KODET, Stefan et al
6 <120> TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
7 NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
8 AND USES THEREOF
10 <130> FILE REFERENCE: CL000891
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C--> 12 <141> CURRENT FILING DATE: 2001-03-13
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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19 <213> ORGANISM: Human
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53 cttggtgaac cgaaatggat ggaacgtgga atatcagatg tgacagacag gaagctgact 1920
54 atggaagaag aggaggccaa gaggatagca gagatgggaa agccagtatt ggggtgaacac 1980

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70 <210> SEQ ID NO: 2

71 <211> LENGTH: 921

72 <212> TYPE: PRT

73 <213> ORGANISM: Human

75 <400> SEQUENCE: 2

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79 20 25 30
80 Gly Gly Ser Gly Asp Val Pro Ser Thr Gly Gln Asn Asn Glu Ser Cys
81 35 40 45
82 Ser Gly Ser Ser Asp Cys Lys Glu Gly Val Ile Leu Pro Ile Trp Tyr
83 50 55 60
84 Pro Glu Asn Pro Ser Leu Gly Asp Lys Ile Ala Arg Val Ile Val Tyr
85 65 70 75 80
86 Phe Val Ala Leu Ile Tyr Met Phe Leu Gly Val Ser Ile Ile Ala Asp
87 85 90 95
88 Arg Phe Met Ala Ser Ile Glu Val Ile Thr Ser Gln Glu Arg Glu Val
89 100 105 110
90 Thr Ile Lys Lys Pro Asn Gly Glu Thr Ser Thr Thr Thr Ile Arg Val
91 115 120 125
92 Trp Asn Glu Thr Val Ser Asn Leu Thr Leu Met Ala Leu Gly Ser Ser
93 130 135 140
94 Ala Pro Glu Ile Leu Leu Ser Leu Ile Glu Val Cys Gly His Gly Phe
95 145 150 155 160
96 Ile Ala Gly Asp Leu Gly Pro Ser Thr Ile Val Gly Ser Ala Ala Phe
97 165 170 175
98 Asn Met Phe Ile Ile Ile Gly Ile Cys Val Tyr Val Ile Pro Asp Gly
99 180 185 190
100 Glu Thr Arg Lys Ile Lys His Leu Arg Val Phe Phe Ile Thr Ala Ala
101 195 200 205
102 Trp Ser Ile Phe Ala Tyr Ile Trp Leu Tyr Met Ile Leu Ala Val Phe
103 210 215 220
104 Ser Pro Gly Val Val Gln Val Trp Glu Gly Leu Leu Thr Leu Phe Phe
105 225 230 235 240

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106 Phe Pro Val Cys Val Leu Leu Ala Trp Val Ala Asp Lys Arg Leu Leu
107          245          250          255
108 Phe Tyr Lys Tyr Met His Lys Lys Tyr Arg Thr Asp Lys His Arg Gly
109          260          265          270
110 Ile Ile Ile Glu Thr Glu Gly Asp His Pro Lys Gly Ile Glu Met Asp
111          275          280          285
112 Gly Lys Met Met Asn Ser His Phe Leu Asp Gly Asn Leu Val Pro Leu
113          290          295          300
114 Glu Gly Lys Glu Val Asp Glu Ser Arg Arg Glu Met Ile Arg Ile Leu
115 305          310          315          320
116 Lys Asp Leu Lys Gln Lys His Pro Glu Lys Asp Leu Asp Gln Leu Val
117          325          330          335
118 Glu Met Ala Asn Tyr Tyr Ala Leu Ser His Gln Gln Lys Ser Arg Ala
119          340          345          350
120 Phe Tyr Arg Ile Gln Ala Thr Arg Met Met Thr Gly Ala Gly Asn Ile
121          355          360          365
122 Leu Lys Lys His Ala Ala Glu Gln Ala Lys Lys Ala Ser Ser Met Ser
123          370          375          380
124 Glu Val His Thr Asp Glu Pro Glu Asp Phe Ile Ser Lys Val Phe Phe
125 385          390          395          400
126 Asp Pro Cys Ser Tyr Gln Cys Leu Glu Asn Cys Gly Ala Val Leu Leu
127          405          410          415
128 Thr Val Val Arg Lys Gly Gly Asp Met Ser Lys Thr Met Tyr Val Asp
129          420          425          430
130 Tyr Lys Thr Glu Asp Gly Ser Ala Asn Ala Gly Ala Asp Tyr Glu Phe
131          435          440          445
132 Thr Glu Gly Thr Val Val Leu Lys Pro Gly Glu Thr Gln Lys Glu Phe
133          450          455          460
134 Ser Val Gly Ile Ile Asp Asp Asp Ile Phe Glu Glu Asp Glu His Phe
135 465          470          475          480
136 Phe Val Arg Leu Ser Asn Val Arg Ile Glu Glu Glu Gln Pro Glu Glu
137          485          490          495
138 Gly Met Pro Pro Ala Ile Phe Asn Ser Leu Pro Leu Pro Arg Ala Val
139          500          505          510
140 Leu Ala Ser Pro Cys Val Ala Thr Val Thr Ile Leu Asp Asp Asp His
141          515          520          525
142 Ala Gly Ile Phe Thr Phe Glu Cys Asp Thr Ile His Val Ser Glu Ser
143          530          535          540
144 Ile Gly Val Met Glu Val Lys Val Leu Arg Thr Ser Gly Ala Arg Gly
145 545          550          555          560
146 Thr Val Ile Val Pro Phe Arg Thr Val Glu Gly Thr Ala Lys Gly Gly
147          565          570          575
148 Gly Glu Asp Phe Glu Asp Thr Tyr Gly Glu Leu Glu Phe Lys Asn Asp
149          580          585          590
150 Glu Thr Val Lys Thr Ile Arg Val Lys Ile Val Asp Glu Glu Glu Tyr
151          595          600          605
152 Glu Arg Gln Glu Asn Phe Phe Ile Ala Leu Gly Glu Pro Lys Trp Met
153          610          615          620
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159          660          665          670
160 Thr Val Asp Lys Leu Ile Lys Lys Thr Asn Leu Ala Leu Val Val Gly
161          675          680          685
162 Thr His Ser Trp Arg Asp Gln Phe Met Glu Ala Ile Thr Val Ser Ala
163          690          695          700
164 Ala Gly Asp Glu Asp Glu Asp Glu Ser Gly Glu Glu Arg Leu Pro Ser
165 705          710          715          720
166 Cys Phe Asp Tyr Val Met His Phe Leu Thr Val Phe Trp Lys Val Leu
167          725          730          735
168 Phe Ala Cys Val Pro Pro Thr Glu Tyr Cys His Gly Trp Ala Cys Phe
169          740          745          750
170 Ala Val Ser Ile Leu Ile Ile Gly Met Leu Thr Ala Ile Ile Gly Asp
171          755          760          765
172 Leu Ala Ser His Phe Gly Cys Thr Ile Gly Leu Lys Asp Ser Val Thr
173          770          775          780
174 Ala Val Val Phe Val Ala Phe Gly Thr Ser Val Pro Asp Thr Phe Ala
175 785          790          795          800
176 Ser Lys Ala Ala Ala Leu Gln Asp Val Tyr Ala Asp Ala Ser Ile Gly
177          805          810          815
178 Asn Val Thr Gly Ser Asn Ala Val Asn Val Phe Leu Gly Ile Gly Leu
179          820          825          830
180 Ala Trp Ser Val Ala Ala Ile Tyr Trp Ala Leu Gln Gly Gln Glu Phe
181          835          840          845
182 His Val Ser Ala Gly Thr Leu Ala Phe Ser Val Thr Leu Phe Thr Ile
183          850          855          860
184 Phe Ala Phe Val Cys Ile Ser Val Leu Leu Tyr Arg Arg Arg Pro His
185 865          870          875          880
186 Leu Gly Gly Glu Leu Gly Gly Pro Arg Gly Cys Lys Leu Ala Thr Thr
187          885          890          895
188 Trp Leu Phe Val Ser Leu Trp Leu Leu Tyr Ile Leu Phe Ala Thr Leu
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195 <211> LENGTH: 126512
196 <212> TYPE: DNA
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199 <220> FEATURE:
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202 <223> OTHER INFORMATION: n = A,T,C or G
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207 tccaagagtg aacctgaagg ctattgttgt tgaaatgtaa taaggagag agtgacggga 180

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3